

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/550, 934  
Source: PCT  
Date Processed by STIC: 10/07/2005

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 10/07/2005

PATENT APPLICATION: US/10/550,934

TIME: 10:11:24

Input Set : A:\14875-151US1.txt

Output Set: N:\CRF4\10072005\J550934.raw

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3 <110> APPLICANT: Tsuchiya, Masayuki
4     Kimura, Naoki
5     Fukuda, Tatsuya
7 <120> TITLE OF INVENTION: MODIFIED ANTIBODIES AGAINST CD22 AND USES THEREOF
9 <130> FILE REFERENCE: 14875-151US1
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/550,934
C--> 11 <141> CURRENT FILING DATE: 2005-09-28
11 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/004696
12 <151> PRIOR FILING DATE: 2004-03-31
14 <150> PRIOR APPLICATION NUMBER: JP 2003-96950
15 <151> PRIOR FILING DATE: 2003-03-31
17 <160> NUMBER OF SEQ ID NOS: 36
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 260
23 <212> TYPE: PRT
24 <213> ORGANISM: Artificial
26 <220> FEATURE:
27 <223> OTHER INFORMATION: an artificially synthesized peptide sequence
29 <400> SEQUENCE: 1
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31 1           5           10           15
33 Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys
34           20           25           30
36 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
37           35           40           45
39 Thr Ser Tyr Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu
40           50           55           60
42 Glu Trp Ile Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn
43 65           70           75           80
45 Gln Asn Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
46           85           90           95
48 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
49           100          105          110
51 Tyr Tyr Cys Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly
52           115          120          125
54 Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Leu
55           130          135          140
57 Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Asn Val Thr
58 145          150          155          160
60 Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ala Asn His Lys
61           165          170          175
63 Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu

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64          180          185          190
66 Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe
67          195          200          205
69 Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Val
70          210          215          220
72 Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln Tyr Leu Ser Ser
73 225          230          235          240
75 Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp
76          245          250          255
78 Asp Asp Asp Lys
79          260
82 <210> SEQ ID NO: 2
83 <211> LENGTH: 810
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial
87 <220> FEATURE:
88 <223> OTHER INFORMATION: an artificially synthesized DNA sequence
90 <220> FEATURE:
91 <221> NAME/KEY: CDS
92 <222> LOCATION: (14)..(799)
95 <400> SEQUENCE: 2
96 cctgaattcc acc atg gaa agg cac tgg atc ttt ctc ttc ctg ttt tca      49
97          Met Glu Arg His Trp Ile Phe Leu Phe Leu Phe Ser
98          1          5          10
100 gta act gca ggt gtc cac tcc cag gtc cag ctg cag gag tca ggg gct      97
101 Val Thr Ala Gly Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Ala
102          15          20          25
104 gaa ctg tca aaa cct ggg gcc tca gtg aag atg tcc tgc aag gct tct      145
105 Glu Leu Ser Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser
106          30          35          40
108 ggc tac acc ttt act agc tac tgg ctg cac tgg ata aaa cag agg cct      193
109 Gly Tyr Thr Phe Thr Ser Tyr Trp Leu His Trp Ile Lys Gln Arg Pro
110 45          50          55          60
112 gga cag ggt ctg gaa tgg att gga tac att aat cct agg aat gat tat      241
113 Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Arg Asn Asp Tyr
114          65          70          75
116 act gag tac aat cag aac ttc aag gac aag gcc aca ttg act gca gac      289
117 Thr Glu Tyr Asn Gln Asn Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp
118          80          85          90
120 aaa tcc tcc agc aca gcc tac atg caa ctg agc agc ctg aca tct gag      337
121 Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu
122          95          100          105
124 gac tct gca gtc tat tac tgt gca aga agg gat att act acg ttc tac      385
125 Asp Ser Ala Val Tyr Tyr Cys Ala Arg Arg Asp Ile Thr Thr Phe Tyr
126          110          115          120
128 tgg ggc caa ggc acc act ctc aca gtc tcc tcg ggt gga ggc ggt agc      433
129 Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser
130 125          130          135          140
132 gac att cag ctg acc cag tct cca tca tct ctg gct gtg tct gca gga      481

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133 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
134                               145                               150                               155
136 gaa aac gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt      529
137 Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
138                               160                               165                               170
140 gca aat cac aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag      577
141 Ala Asn His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
142                               175                               180                               185
144 tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc      625
145 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
146                               190                               195                               200
148 cct gat cgc ttc aca ggc agc gga tct ggg aca gat ttt act ctt acc      673
149 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
150 205                               210                               215                               220
152 atc agc aga gta caa gtt gaa gac ctg gca att tat tat tgt cac caa      721
153 Ile Ser Arg Val Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln
154                               225                               230                               235
156 tac ctc tcc tcg tgg acg ttc ggt gga ggg acc aag ctg gag atc aaa      769
157 Tyr Leu Ser Ser Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
158                               240                               245                               250
160 gac tac aag gat gac gac gat aag tga taa gcggccgcaa t      810
161 Asp Tyr Lys Asp Asp Asp Asp Lys
162                               255                               260
165 <210> SEQ ID NO: 3
166 <211> LENGTH: 262
167 <212> TYPE: PRT
168 <213> ORGANISM: Artificial
170 <220> FEATURE:
171 <223> OTHER INFORMATION: an artificially synthesized peptide sequence
173 <400> SEQUENCE: 3
174 Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu Thr Leu Lys Gly
175 1                               5                               10                               15
177 Val Lys Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
178                               20                               25                               30
180 Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe
181                               35                               40                               45
183 Ser Ile Tyr Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu
184                               50                               55                               60
186 Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro
187 65                               70                               75                               80
189 Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
190                               85                               90                               95
192 Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met
193                               100                              105                              110
195 Tyr Tyr Cys Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu
196                               115                              120                              125
198 Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala Gly Gly
199                               130                              135                              140
201 Gly Gly Ser Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala

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202 145          150          155          160
204 Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile
205          165          170          175
207 Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys
208          180          185          190
210 Leu Leu Ile Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Lys
211          195          200          205
213 Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn
214          210          215          220
216 Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr
217 225          230          235          240
219 Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr
220          245          250          255
222 Lys Asp Asp Asp Asp Lys
223          260
226 <210> SEQ ID NO: 4
227 <211> LENGTH: 816
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial
231 <220> FEATURE:
232 <223> OTHER INFORMATION: an artificially synthesized DNA sequence
234 <220> FEATURE:
235 <221> NAME/KEY: CDS
236 <222> LOCATION: (14)..(805)
239 <400> SEQUENCE: 4
240 cctgaattcc acc atg aac ttt ggg ctc aga ttg att ttc ctt gtc ctt      49
241          Met Asn Phe Gly Leu Arg Leu Ile Phe Leu Val Leu
242          1          5          10
244 act tta aaa ggt gtg aag tgt gaa gtg cag ctg gtg gag tct ggg gga      97
245 Thr Leu Lys Gly Val Lys Cys Glu Val Gln Leu Val Glu Ser Gly Gly
246          15          20          25
248 ggc tta gtg aag cct gga ggg tcc ctg aaa ctc tcc tgt gca gcc tct      145
249 Gly Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser
250          30          35          40
252 gga ttc gct ttc agt atc tat gac atg tct tgg gtt cgc cag act ccg      193
253 Gly Phe Ala Phe Ser Ile Tyr Asp Met Ser Trp Val Arg Gln Thr Pro
254 45          50          55          60
256 gag aag agg ctg gag tgg gtc gca tac att agt agt ggt ggt ggt acc      241
257 Glu Lys Arg Leu Glu Trp Val Ala Tyr Ile Ser Ser Gly Gly Gly Thr
258          65          70          75
260 acc tac tat cca gac act gtg aag ggc cga ttc acc atc tcc aga gac      289
261 Thr Tyr Tyr Pro Asp Thr Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
262          80          85          90
264 aat gcc aag aac acc ctg tac ctg caa atg agc agt ctg aag tct gag      337
265 Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu
266          95          100          105
268 gac aca gcc atg tat tac tgt gca aga cat agt ggc tac ggt agt agc      385
269 Asp Thr Ala Met Tyr Tyr Cys Ala Arg His Ser Gly Tyr Gly Ser Ser
270          110          115          120

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272 tac ggg gtt ttg ttt gct tac tgg ggc caa ggg act ctg gtc act gtc      433
273 Tyr Gly Val Leu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
274 125                      130                      135                      140
276 tct gca ggt gga ggc ggt agc gat atc cag atg acc cag act aca tcc      481
277 Ser Ala Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Thr Thr Ser
278                      145                      150                      155
280 tcc ctg tct gcc tct ctg gga gac aga gtc acc att agt tgc agg gca      529
281 Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala
282                      160                      165                      170
284 agt cag gac att agc aat tat tta aac tgg tat cag cag aaa cca gat      577
285 Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp
286                      175                      180                      185
288 gga act gtt aaa ctc ctg atc tac tac aca tca ata tta cac tca gga      625
289 Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Ile Leu His Ser Gly
290 190                      195                      200
292 gtc cca tca aag ttc agt ggc agt ggg tct gga aca gat tat tct ctc      673
293 Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu
294 205                      210                      215                      220
296 acc att agc aac ctg gag caa gaa gat ttt gcc act tac ttt tgc caa      721
297 Thr Ile Ser Asn Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln
298                      225                      230                      235
300 cag ggt aat acg ctt ccg tgg acg ttc ggt gga ggc acc aag ctg gaa      769
301 Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu
302                      240                      245                      250
304 atc aaa gac tac aag gat gac gac gat aag tga taa gcggccgcaa t      816
305 Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys
306                      255                      260
310 <210> SEQ ID NO: 5
311 <211> LENGTH: 116
312 <212> TYPE: PRT
313 <213> ORGANISM: Artificial
315 <220> FEATURE:
316 <223> OTHER INFORMATION: an artificially synthesized peptide sequence
318 <400> SEQUENCE: 5
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320 1                      5                      10                      15
322 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
323                      20                      25                      30
325 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
326                      35                      40                      45
328 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe
329                      50                      55                      60
331 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
332 65                      70                      75                      80
334 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
335                      85                      90                      95
337 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu
338                      100                     105                     110
340 Thr Val Ser Ser

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RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 10/07/2005  
PATENT APPLICATION: US/10/550,934      TIME: 10:11:25

Input Set : A:\14875-151US1.txt  
Output Set: N:\CRF4\10072005\J550934.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27

Seq#:28,29,30,31,32,33,34,35,36

**VERIFICATION SUMMARY**

DATE: 10/07/2005

PATENT APPLICATION: US/10/550,934

TIME: 10:11:25

Input Set : A:\14875-151US1.txt

Output Set: N:\CRF4\10072005\J550934.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date